Amendment to the Claims:

This listing of the claims will replace all prior versions, and listings, of the claims in the application:

Listing of the Claims:

1-73. (Cancelled)

74. (Original) A method of preparing a therapeutic agent comprising the formula I-L-P', wherein I is an immunoglobulin heavy chain constant region or fragment thereof that retains the ability to bind an Fc receptor; L is a linker group or a direct bond; and
P' is a peptide capable of binding a target protein, the method comprising:

(1) screening a peptide library to identify one or more peptides which bind to the target protein;

(2) determining the amino acid sequence of at least one peptide which binds to the target protein; and

(3) producing a therapeutic agent comprising a peptide having the amino acid sequence identified in step (2), an immunoglobulin heavy chain constant region or fragment thereof that retains the ability to bind an Fc receptor, and a linker group or a direct bond.

75. (Original) The method of claim 74, wherein the peptide library comprises L-amino acid peptides.

76. (Original) The method of claim 74, wherein the peptide library comprises D-amino acid peptides.

77-78. (Cancelled)

79. (New) The method of claim 74, wherein the target protein is associated with a pathogenic organism.

80. (New) The method of claim 79, wherein the protein associated with a pathogenic organism is a membrane-associated protein.

81. (New) The method of claim 80, wherein said membrane-associated protein is a viral coat protein.

82. (New) The method of claim 80, wherein said membrane-associated protein is a bacterial membrane protein.

83. (New) The method of claim 74, wherein said target protein is a surface protein of an aberrant cell.

84. (New) The method of claim 83, wherein said aberrant cell is a cell that exhibits unregulated proliferation.

85. (New) The method of claim 84, wherein said cell that exhibits unregulated cell proliferation is a cancer cell.

86. (New) The method of claim 84, wherein said target protein is a protein that is associated with a disease state.

87. (New) The method of claim 85, wherein said protein that is associated with a disease state is a toxin molecule.

88. (New) The method of claim 87, wherein said toxin molecule is a viral toxin.

89. (New) The method of claim 85, wherein said toxin molecule is a bacterial toxin.

90. (New) The method of claim 89, wherein said bacterial toxin is selected from the group consisting of *C. difficile* toxin A and *C. difficile* toxin B.

91. (New) The method of claim 89, wherein said bacterial toxin is a pathogenic toxin produced by *E. coli*.

92. (New) The method of claim 74, wherein said P wherein P is a peptide capable of binding an amyloidogenic protein selected from the group consisting of transthyretin (TTR), prion protein (PrP), islet amyloid polypeptide (IAPP), atrial natriuretic factor (ANF), kappa light

chain, lambda light chain, amyloid A, procalcitonin, cystatin C, β2 microglobulin, ApoA-I, gelsolin, calcitonin, fibrinogen and lysozyme.

93. (New) The method of claim 92, wherein P comprises a subregion of an amyloidogenic protein selected from the group consisting of transthyretin (TTR), prion protein (PrP), islet amyloid polypeptide (IAPP), atrial natriuretic factor (ANF), kappa light chain, lambda light chain, amyloid A, procalcitonin, cystatin C, β2 microglobulin, ApoA-I, gelsolin, calcitonin, fibrinogen and lysozyme.

94. (New) The method of claim 74, wherein P is a fragment of β-AP that is capable of binding an amyloidgenic protein.

95. (New) The method of claim 94, wherein said fragment of β-AP is selected from the group consisting of $A\beta_{16-30}$, $A\beta_{17-20}$, $A\beta_{17-21}$, $A\beta_{16-25}$, and $A\beta_{1-25}$.

96. (New) The method of claim 74, wherein P is a peptide comprising the structure

(Y-Xaa_1-Xaa_2-Xaa_3-Xaa_4-Z)

wherein Xaa_1, Xaa_2, Xaa_3 and Xaa_4 are each D-amino acid structures and at least two of Xaa_1, Xaa_2, Xaa_3 and Xaa_4 are, independently, selected from the group consisting of a D-leucine structure, a D-phenylalanine structure and a D-valine structure;

Y, which may or may not be present, is a structure having the formula $(Xaa)_a$, wherein Xaa is any D-amino acid structure and a is an integer from 1 to 15; and

Z, which may or may not be present, is a structure having the formula $(Xaa)_b$, wherein Xaa is any D-amino acid structure and b is an integer from 1 to 15.

97. (New) The method of claim 74, wherein P is a peptide selected from the group consisting of: D-Leu-D-Val-D-Phe-D-Phe, D-Leu-D-Val-D-Phe-phenethylamide, D-Leu-D-Val-D-Tyr-D-Phe, D-Leu-D-Val-D-IodoTyr-D-Phe, D-Leu-D-Val-D-Phe-D-Tyr, D-Leu-D-Val-D-Phe-D-IodoTyr, D-Leu-D-Val-D-Phe-D-Ala, D-Leu-D-Val-D-Phe-D-Phe-D-Ala, D-Ala-D-Val-D-Phe-D-Phe-D-Leu, D-Leu-D-Val-D-Tyr-D-Phe-D-Ala, D-Leu-D-Val-D-IodoTyr-D-Phe-D-Ala, D-Leu-D-Val-D-Phe-D-Tyr-D-Ala, D-Leu-D-Val-D-Phe-D-IodoTyr-D-Ala, D-Phe-D-Phe-D-Val-D-Leu, D-Ala-D-Phe-D-Phe-D-Val, D-Ala-D-Phe-D-Phe-D-Val-D-Leu, D-Ala-D-Phe-D-Phe-D-Leu-D-Leu, D-Leu-D-Phe-D-Phe-D-Val-D-Leu, D-Phe-D-Phe-D-Phe-D-Val-D-Leu, D-Phe-D-Phe-D-Phe-D-Leu-D-Val, D-Phe-D-Phe-D-Phe-D-Phe-D-Leu, D-Ala-D-Phe-D-Phe-D-Phe-D-Leu, Aβ(16-30), Aβ(10-25), Aβ(1-29), Aβ(1-40), and Aβ(1-42).

98. (New) The method of claim 74, wherein said therapeutic agent is Aβ(16-30)-hFc.